

FIGURE 1A - 1

1 M A L R R S M G R P G L P P L P P P R L G L L L A A L A S
 1 CCCCGATGG CGCTGAGGG GAGCATGGGG CGGGCCGGGC TCCCGGCGCT GCGCGTGGCC CGGCCACCGC GGCTCGGGCT GCTCTGGCT
 33 L L L P E S A A G L M G A P V K L T V S Q G Q P V K L N C S
 101 CTCGTGCTGC CCCGGAGTCC GCGGCCGAG TGCTGAAGCT CATGGAGCC CGGGTGAGG TGACAGTGTGTC TCAGGGCG AGCGTAAGC TCAACTGGAG
 66 V E G M E E P D I Q W V K D G A V V Q N L D Q L Y I P V S E Q H W
 201 TGTGGAGGG ATGGAGGGC CTGACATCCA GTGGGTGAAG GATGGGGCTG TGTTCCAGM CTGGACCAAG TTGTACATCC CAGTCAGGA CGAGCACTGG
 99 I G F L S L K S V E R S D A G R Y W C Q V E D G G E T E I S Q P V W
 301 ATGGCTTCC TCAGGCTGAA GTCAAGTGGAG CGGCTCTGACG CCGGGCTGGTA CTGGTCCAG GTGGAGGATG GGGGTAAAC CGAGATCTCC CAGCCAGTGT
 133 L T V E G V P F F T V E P K D L A V P P N A P F Q L S C E A V G P
 401 GGCTCACGGT AGAAGGTGTG CCATTTCAC CAGTGGAGCC AAAGATCTG GCAGTGGCCAC CCAGTGGCCAC TTTCCAACCTG TCTTGTGAGG CTGTGGGTCC
 166 P E P V T I V W W R G T T K I G G P A P S P S V L N V T G V T Q S
 501 CCCGTAAACT GTTACCATG TCTGGATGG AGGAACATGAG AAGATGGGG GACCGCTCC CTCTCCATCT GTTTAAATG TAACAGGGGT GACCCAGAGC
 199 T M F S C E A H N L K G L A S S R T A T V H L Q A L P A A P F N I T
 601 ACCATGTTT CCTGTGAAGC TCACAACCTA AAAGGCCTGG CCTCTCTCG CACAGCCACT GTCACCTTC AAGCACTGCC TGCAACCTCA
 233 V T K L S S S N A S V A W M P G A D G R A L L Q S C T V Q V T Q A
 701 CCGTGACAAA GCTTTCCAGC AGCAACGCTA GTGGGGCTG GATGGCAGGT GCTGTATGGCC GAGCTCTGCT ACAGTTCAGG TGACACAGGC
 266 P G G W E V L A V V V P V P P F T C L L R D L V P A T N Y S L R V
 801 CCCAGGAGGC TGGGAAGTCC TGGCTGTTGT GGTCCCTGTG CCCCCCTTA CCTGCTGTGCT CGGGGACCTG GTGCCTGCCA CCAACTACAG CCTCAGGGTG
 299 R C A N A L G P S P Y A D W V P F Q T K G L A P A S A P Q N L H A I
 901 CGCTGTGCCA ATGCCCTGGG GCCCTCTCCC TATGCTGACT GGTTGCCCTT TAGACCAAG GGCTCTGCC CAGCCAGGGC TCCCCAAAAC CTCCATGCCA
 333 R T D S G L I L E W E V I P E A P L E G P L G P Y K L S W V Q D
 1001 TCCGCACAGA TTCAAGCTC ATCTGGAGT GGGAGAGT GATCTGGAGT GGGAGAGT GGGCCCCGGAS GGGCCCCCTTGG AAGGGCCCCCTTGG GGGACCCATACAG CCTCAGGGTG
 * Q D E L T V E G T R A N L T G W D P Q K D L I V R V C V S N
 1101 CAATGGAAACC CAGGATGAGG TGACAGTGGAG GCGGACCCAGG GCCAATTGTA CAGGTGGGA TCCCCAAAAG GACCTGATCG TACGTGTGTG CGTCTCCAAT
 399 A V G C G P W S Q P L V V S H D R A G Q Q G P P H S R T S W V P V
 1201 GCAGTTGGCT GTGGACCCCTG GAGTCAGCCA CTGGTGTCT CTCCTCATGA CCGTCAGGC CAGCAGGGCC CTCCTCACAG CGGCACTCC TGGGTACCTG

433 V L G V L T A L V T A A A L I L L R K R R K E T R F G Q A F D
 1301 TGGCTCTGG TGTGCTAACG GCGCTGGTA CGCTGGCTGC CCTGGCTGC ATCCTGGCTC GAAAGAGACG CGGTTGGGC AAGGCTTTGA

FIGURE 1A-2

466 S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L
 1401 CAGTGTCTATGCCGGAGCCCCGGT TCACTTCGGG GCAGCCGGT CCTTCATCG AGAACGGCC GAGGCATCG AGGCCACATT GGACAGCTTG
 499 G I S D E L K E K L E D V L I P E Q Q F T L G R M L G K G E F G S V
 1501 GGCACTCGGG ATGAACTAAA GGAAAGACTG GAGGATGTGC ACAGCAGTTGACGAGGGTGGG CAAAGGAGAG TTGGTGTTCAG
 533 R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E F
 1601 TGGGGAGGC CCAGCTTGA TGAGGAGG CAAGGGATG GCTCCCTTGT GAAAGTGGCT GTGAGATGCA CATCATGCC TCAAAGGACA TTGAAGAGTT
 566 L R E A A C W K E F D H P H V A K L V G V S L R S R A K G R L P I
 1701 CCTCAGGAA GCAGCTTCA TGAGGAGT CACCATCCN CACGGCTCA AAATGTTGG GTAAAGCTG TGAAAGCTC CGGAGGAGG CTAAAGGCCG TCTCCCCCATC
 599 P M V I L P F M K H G D L H A F L L A S R I G E N P F N L P L Q T L
 1801 CCCATGGTCA TCTTGGCCCTT CATGAAAGCAT GGGGACCTGC ATGCCCTCTT GCTGAGCTCT CGGAGCTCC CCGATTTGGG AGAACCCCTT TAACCTACCC CTCCAGACCC
 633 I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A E
 1901 TGATCCGGTT CATGGTGGAC ATTGGCTGG GCATGGAGTA CCTGAGCTCT CGGAACCTCA TCCACCGAGA CCTGGCTGCT CGGAATTGCA TGCTGGCAGA
 666 D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K W
 2001 GGACATGACA GTGTGTGG CTGACTTCGG ACTCTCCGG AAGATCTACA GTGGGACTA CTATCGTCAA GGCTGTGCCT CCAAACGTGCC TGTCAAAGTGG
 699 L A L E S L A D N L Y T V Q S D V W A F G V T M W E I M T R G Q T P
 2101 CTGGCCCTGG AGAGCCTGG CGACACCTG TATACTGTGC AGAGTGAAGT GTGGGTGACCA TGTGGAGAT CATGACACGT GGGCAGACGC
 733 Y A G I E N A E I Y N Y L I G G N R L K Q P P E C M E D V Y D L M
 2201 CATATGCTGG CATGAAAAAC GCTGAGGATT ACAACTACCT CATGGGGG AACCGCCTGA AACAGCCTCC GGAGTGTATG GAGGACGTGT ATGATCTCAT
 766 Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A
 2301 GTACCACTGC TGGAGTGC CCTTATACTAT CAACATCGAG AGAGCTGAG AGCCCAGCA CGCCCGAGC TTTACTTGTCTG TGGAATGGA ACTGGAGAAC ATCTGGGCC AGCTGTCTGT GCTATCTGCC
 799 S Q D P L Y I N I E R A E E P T A G G S L E L P G R D Q P Y S G A G
 2401 AGCCAGGACC CCTTATACTAT CAACATCGAG AGAGCTGAG AGCCCAGCA CGCCCGAGC TACNTACTCA CCCCCGGAG GCTGGAGCTAC TCAGCCCTAC AGTGGGGCTG
 833 D G S G M G A V G G T P S D C R Y I L T P G G L P H S S C O
 2501 GGGATGGCAG TGGCATGGG GCACTGGGTG GAGGACACA GAGGCTTGTG TGACTGTGG TACNTACTCA CCCCCGGAG GCTGGAGCTAC CCACAGGCAG AGGGCATCG
 866 Q P E S P L N E T Q R L L L Q Q G L L P H S S C O
 2601 CCAGCCAGAG AGTCCCTCA ATGAGACACA GAGGCTTGTG CTGCTGGAG AAGGGCTACT GCCACACAGT AGCTGTGTAGC CCACAGGCAG AGGGCATCG
 2701 GGCCATTGG CGGGCTCTGG TGGCCACTGA TAAGCCCCGT CTGACCCAG CCCAGACAGC AAGGTGTGGA GGCTCCTGTG GTAGTCCTCC
 2801 CAACCTGTGC TGGAAAGCC GGAACGCA ACCMTCACCA TCCCAGTCTCT TCCCTGCAACC AGTCTGTGCC CAGCCTGGCA TCAGTTTAGG CCTTGGCTGG

FIGURE 1A-3

2901 ATGGAAGTGG GCCAGTCCTG GTTGTCTGAA CCCAGGCAGC TGGCAGGAGT GGGGTGGTTA TGTTTCCATG GTTACCATGG GTGTGGATGG CAGTGTGGGG
3001 AGGGCAAGTC CAGCTCTGTG GGCCTTAACCC TCCTGCTGAG CTGCCCTCTGC TGCTTAAGTG CATGCATGA GCTGCCTCCA GCCTGGTGGC CCAGCTTATA
3101 CCACACTTGG GTTTAAATA TCCAGGTGTG CCCCTCCAAAG TCACAAAGAG ATGTCCTTGT AAATATTCCCT TTAGGTGAG GGTGGTAAG GGGTTGGTAT
3201 CTAGGGTCTG AATCTTCACC ATCTTCTCTGA TTCCGGCACCC TGCCTACGCC AGGAGAACGTT GAGGGGGAGCA TGCTTCCCTG CAGCTGACCCG GGTACACCAA
3301 AGGCATGCTG GAGTACCCAG CCTATCAGGT GCCCTCTTC CAAAGGCAGC GTGCCGAGCC AGCAAGAGGA AGGGGTGCTG TGAGGCTGTGC CCAGGGAGCAA
3401 GTGAGGCCGG AGAGGAGTTG AGGAACCCCTT CTCCATACCC ACAATCTGAG CACCGTACCA AATCTAAAAA TATCTTAAGA CTAACAAAGG CAGCTGTGTC
3501 TGAGCCCAAC CCTTCTAAAC GGTGACCTT AGTGCCTAACT TCCCCTCTAA CTGGACAGCC TCTTCTGTCC CAAGTCTCCA GAGAGAAATC AGGCTGTGATG
3601 AGGGGGAAATT C

FIGURE 1B-1

FIGURE 1B-2

FIGURE 1B-2
 481 I E A T L D S L G I S D E L K E K L E D V L I P E Q Q F T L G R M
 1501 CATTGAGGCC ACATGGATA GCCTGGCAT CAGCGATGAA TTGAAGAAA AGCTGGAGGA TGTCTCTCAT CCAGAGGAGC AGTTACCCCT CGGTCGGATC
 514 A S S D I E E F L R E A A C M K E F D H P H V A K L V G V S L R S
 1701 TTGGCAAG GAGAGTGG ATCAGTGGGG MAAGCCAGG TAAGCAGGA AGATGGCTCC TTCTGTGAAG TGGCAGTGAAT GATGCTGAAA GCTGACATCA
 548 R A K G R L P I P M V I L P F M K H G D L H A F L L A S R I G E N
 1801 CAGGCTAA GGTCCTTC CCATTCCAT GCTCATCCCTG CCCTTCATGAA AACATGGAGA CCTTCGACGCC TTTCCTGCTCG CCTTCGAAAT CGGGGAGAAC
 581 P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A
 1901 CCCCCAACCGCCCTGCA GACCTCTGGC CGGCTCTGGC TGCGCATTTGC CTGCGCTTG GAGTACCTGA GCTTCCGGMA CTTCATCCAC CGAGACCTG
 614 A R N C M L A E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C
 2001 CAGCTGGAA TTGCTATGCTG GCGAGGACA TGACAGTGTG TCTGGACTCT CTGGCTGAT TTGGACTCT CTCGGAAAT CTATAGCGGG GACTATTATC GTCAAGGGCTG
 648 A S K L P V K W L A L E S L A D N L Y T V H S D V W A F G V T M W
 2101 TGCCCTCAA TTGCCCCATCA AGTGGCTGGC TTGGCTGACA ACTTGATATAC TGTAACACAGT GATGTTGGG CCTTCGGGT GACCATGTTGG
 681 E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K Q P P E C
 2201 GAGATCATCA CTCGGGGCA GACGCCATAT GCTGGCATG AAAATGCTGA GATTACAAC TRACCTCATCG GCGGGAAACCG CCTGAAGGAG CCTCCGGAGT
 714 M E E V Y D L M Y Q C W S A D P K Q R P S F T C L R M E L E N I L
 2301 GCATGGGGAA AGTGTATGAT CTATGTACC AGTGCTGGAG CGCGGACCCC AAAGCGGGCC CAAGCTTCAC GTGTCTGGGA ATGCAACTGG AGAACATCT
 748 G H L S V L S T S Q D P L Y I N I E R A E Q P T E S G S P E L H C
 2401 GGGCCACCTG TCTGTGCTG TACATCAACA TTGGAGAGGC TGAGCAGGCT ACTGAGAGTG GCAGCCCTGA GCTGCACTGT
 781 G E R S S S E A G D G S G V A V G G I P S D S R Y I F S P G G L S
 2501 GGAGAGGGAT CCAGCAGGCA GGAGGGGAC CCAAAGGCC CCTCAATGAG AACAGAGGC TGTGTGTGCT GCAGCAAGGG CTACTGCCTC ACAGTAGCTG
 814 O
 2701 TTAACTTCA GGCAGAGGA AGTTGGGGCC CCTGGCTCTG CTGACCGCTG CGTGGCCAG TCTGATACA GCCAGGGAG CAAGGTATGG
 2801 AGGTCTGT GGTAACCTC CCAAGCTGTG TGGGCCCTGG ACGGACCAA TTGCCCCATC CCAGTCTTC CTGAGCCGC TCTGGCATCAG
 848 E S P G Q L E Q Q P E S P L N E N Q R L L L Q Q G L L P H S S C
 2601 CCGAGTACCC AGGGCAGCTG GAGCAGGAGC CAGAAAGGCC CCTCAATGAG AACAGAGGC TGTGTGTGCT GCAGCAAGGG CTACTGCCTC ACAGTAGCTG
 881
 2701
 2801
 2901
 3001

FIGURE 1B - 3

3201 AGGAAGGGAT TGGCACACTT GGGTCCCTAA GCCCTATGGC AGGAAATGGT GGATATTCT CAGGTCTGAA TCCTCATCAT CTTCCTGATT CCCACCCCTG
3301 CAAAGGCCTG GAACCTGGCTG TGGGGCTCTG ACACCATGCTG AAGGATGCTG AGCGATGCTG AAGGACAAAA GGTACAGAG ATCCGACTTC AAAAGGCAGG GTCTGAGTCT GTCTGAGTCT GGCAGGTGGA
3401 GAGGTGCTAA GGGGCTGGCC CAGGAGTCAG GCATTTCAAG ACCCCCTCAA GCTTCTACAG TCTGTCAG CATGCTACCA AGCCCCAGA TACCCAAAA
3501 CTAACAGAGG CAGTTCATGTC TGAGGCCAGC CCTCCACAT GATGACCTT AGGTCTACCC TCCTCTCTAA ATGGACATCC TGTTTGTC CCAGTCTCCA
3601 GAGAGACTAC TGATGGCTGA TGTGGGTAAG AAAAGTTCCA GGAACCAAGGG CTGGGGTGG ACCAGGGCTG GGGTCGAGGC AGGCTCTGG GCAGGGCTCTT
3701 GCTCTAGGA ACATTTCTAA GCTTAAAGT TGCTGTTCA AACAAATAA ATTGAACA TAAAGATAA AAAA

FIGURE 2 -1

1 GAATTCTCGA GTCGACGTTG GACTTGAAGG AATGCCAAGA GATGCTGCC
 51 CCACCCCTT AGGCCGAGG GATCAGGAGC TATGGGACCA GAGGCCCTGT
 1 MetGlyPro GluAlaLeuSer

 101 CATCTTACT GCTGCTGCTC TTGGTGGCAA GTGGAGATGC TGACATGAAG
 8 SerLeuLe uLeuLeuLeu LeuValAlaS erGlyAspAl aAspMetLys

 151 GGACATTTG ATCCCTGCCAA GTGCCGCTAT GCCCTGGGCA TGCAGGGACCG
 24 GlyHisPheA spProAlaLy sCysArgTyr AlaLeuGlyM etGlnAspArg
 201 GACCACATCCCCA GACAGTGACA TCTCTGCTTC CAGCTCCTGG TCAGATTCCA
 41 ThrIlePro AspSerAspI leSerAlaSe rSerSerTrp SerAspSerThr
 251 CTGCCGCCCG CCACAGCAGG TTGGAGAGCA GTGACGGGGA TGGGGCCTGG
 58 AlaAlaAr gHisSerArg LeuGluSerS erAspGlyAs pGlyAlaTrp
 301 TGCCCCGCAG GGTGGTGTGTT TCCCAAGGAG GAGGAGTACT TGCAGGGTGG
 74 CysProAlaG lySerValPh eProLysGlu GluGluTyrL euGlnValAsp
 351 TCTACAAACGA CTGCACCTGG TGGCTCTGGT GGGCACCCAG GGACGGCATG
 91 LeuGlnArg LeuHisLeuV alAlaLeuVa 1GlyThrGln GlyArgHisAla
 401 CCGGGGGCCT GGGCAAGGAG TTCTCCCGGA GCTACCGGCT GCGTTACTCC
 108 GlyGlyLe uGlyLysGlu PheSerArgS erTyrArgLe uArgTyrSer
 451 CGGGATGGTC GCCGCTGGAT GGGCTGGAAG GACCGCTGGG GTCAGGGAGGT
 124 ArgAspGlyA rgArgTrpMe tGlyTrpLys AspArgTrpG lyGlnGluVal
 501 GATCTCAGGC AATGAGGACC CTGAGGGAGT GGTGCTGAAG GACCTTGGC
 141 IleSerGly AsnGluAspP roGluGlyVa lValLeuLys AspLeuGlyPro
 551 CCCCATGGT TGCCCGACTG GTTCGCTTCT ACCCCCCGGC TGACCGGGTC
 158 ProMetVa lAlaArgLeu ValArgPheT yrProArgAl aAspArgVal
 601 ATGAGCGTCT GTCTGCGGGT AGAGCTCTAT GGCTGCCTCT GGAGGGATGG
 174 MetSerValC ysLeuArgVa 1GluLeuTyr GlyCysLeuT rpArgAspGly
 651 ACTCCTGTCT TACACCGCCC CTGTGGGCA GACAATGTAT TTATCTGAGG
 191 LeuLeuSer TyrThrAlaP roValGlyG1 nThrMetTyr LeuSerGluAla
 701 CCGTGTACCT CAACGACTCC ACCTATGACG GACATACCGT GGGCGGACTG
 208 ValTyrLe uAsnAspSer ThrTyrAspG lyHisThrVa 1GlyGlyLeu
 751 CAGTATGGGG GTCTGGGCCA GCTGGCAGAT GGTGTGGTGG GGCTGGATGA
 224 GlnTyrGlyG lyLeuGlyG1 nLeuAlaAsp GlyValValG lyLeuAspAsp
 801 CTTTAGGAAG AGTCAGGAGC TGCAGGCTG GCCAGGCTAT GACTATGTGG
 241 PheArgLys SerGlnGluL euArgValTr pProGlyTyr AspTyrValGly
 851 GATGGAGCAA CCACAGCTTC TCCAGTGGCT ATGTGGAGAT GGAGTTTGAG
 258 TrpSerAs nHisSerPhe SerSerGlyT yrValGluMe tGluPheGlu

FIGURE 2 - 2

901 TTTGACCGGC TGAGGGCCTT CCAGGCTATG CAGGTCCACT GTAACAAACAT
 274 PheAspArgL euArgAlaPh eGlnAlaMet GlnValHisC ysAsnAsnMet

951 GCACACGCTG GGAGCCCCGTC TGCCTGGCGG GGTGGAATGT CGCTTCCGGC
 291 HisThrLeu GlyAlaArgL euProGlyGl yValGluCys ArgPheArgArg

1001 GTGGCCCTGC CATGGCCTGG GAGGGGGAGC CCATGCCCA CAACCTAGGG
 308 GlyProAl aMetAlaTrp GluGlyGluP roMetArgHi sAsnLeuGly

1051 GGCAACCTGG GGGACCCCAG AGCCCGGGCT GTCTCAGTGC CCCTTGGCGG
 324 GlyAsnLeuG lyAspProAr gAlaArgAla ValSerValP roLeuGlyGly

1101 CCGTGTGGCT CGCTTTCTGC AGTGCCGCTT CCTCTTTGCG GGGCCCTGGT
 341 ArgValAla ArgPheLeuG lnCysArgPh eLeuPheAla GlyProTrpLeu

1151 TACTCTTCAG CGAAATCTCC TTCATCTCTG ATGTGGTGAA CAATTCTCT
 358 LeuPheSe rGluIleSer PheIleSerA spValValAs nAsnSerSer

1201 CCGGCACTGG GAGGCACCTT CCCGCCAGCC CCCTGGTGGC CGCCTGGCCC
 374 ProAlaLeuG lyGlyThrPh eProProAla ProTrpTrpP roProGlyPro

1251 ACCTCCCACC AACTTCAGCA GCTTGGAGCT GGAGCCCAGA GGCCAGCAGC
 391 ProProThr AsnPheSerS erLeuGluLe uGluProArg GlyGlnGlnPro

1301 CCGTGGCCAA GCCCGAGGGG AGCCCGACCG CGATCCTCAT CGGCTGCCTG
 408 ValAlaLy sProGluGly SerProThrA laIleLeuIl eGlyCysLeu

1351 GTGCCATCA TCCTGCTCCT GCTGCTCATC ATTGCCCTCA TGCTCTGGCG
 424 ValAlaIleI leLeuLeuLe uLeuLeuIle IleAlaLeuM etLeuTrpArg

1401 GCTGCACTGG CGCAGGCTCC TCAGCAAAGGC TGAAACGGAGG GTGTTGGAAG
 441 LeuHisTrp ArgArgLeuL euSerLysAl aGluArgArg ValLeuGluGlu

1451 AGGAGCTGAC GGTTCACCTC TCTGTCCCTG GGGACACTAT CCTCATCAAC
 458 GluLeuTh rValHisLeu SerValProG lyAspThrIl eLeuIleAsn

1501 AACCGCCCAG GTCCTAGAGA GCCACCCCCG TACCAGGAGC CCCGGCCTCG
 474 AsnArgProG lyProArgGl uProProPro TyrGlnGluP roArgProArg

1551 TGGGAATCCG CCCCCACTCCG CTCCCTGTGT CCCCCATGGC TCTGCGTTGC
 491 GlyAsnPro ProHisSerA laProCysVa lProAsnGly SerAlaLeuLeu

1601 TGCTCTCCAA TCCAGCCTAC CGCCTCCTTC TGGCCACTTA CGCCCGTCCC
 508 LeuSerAs nProAlaTyr ArgLeuLeuL euAlaThrTy rAlaArgPro

1651 CCTCGAGGCC CGGGCCCCCCC CACACCCGCC TGGGCCAAC CCACCAACAC
 524 ProArgGlyP roGlyProPr oThrProAla TrpAlaLysP roThrAsnThr

1701 CCAGGCCTAC AGTGGGGACT ATATGGAGCC TGAGAAGCCA GGCAGCCCCGC
 541 GlnAlaTyr SerGlyAspT yrMetGluPr oGluLysPro GlyAlaProLeu

1751 TTCTGCCCTAC ACCTCCCCAG AACAGCGTCC CCCATTATGC CGAGGCTGAC
 558 LeuProPr oProProGln AsnSerValP roHisTyrAl aGluAlaAsp

FIGURE 2-3

1801 ATTGTTACCC TGCAGGGCGT CACCGGGGGC AACACCTATG CTGTGCCCTGC
 574 IleValThrL euGlnGlyVa 1ThrGlyGly AsnThrTyrA laValProAla

 1851 ACTGCCCTCAAG GGGCGAGTCG GGGATGGGCC CCCCCAGAGTG GATTCCCTC
 591 LeuProPro GlyAlaValG lyAspGlyPr oProArgVal AspPheProArg

 1901 GATCTCGACT CCGCTTCAAG GAGAACGTTG GCGAGGGCCA GTTGGGGAG
 608 SerArgLe uArgPheLys GluLysLeuG lyGluGlyGl nPheGlyGlu
 << <

 1951 GTGCACCTGT GTGAGGTCGA CAGCCCTCAA GATCTGGTCA GTCTTGATTT
 624 ValHisLeuC ysGluValAs pSerProGln AspLeuValS erLeuAspPhe

 2001 CCCCTTAAT GTGCGTAAGG GACACCCTT GCTGGTAGCT GTCAAGATCT
 641 ProLeuAsn ValArgLysG lyHisProLe uLeuValAla ValLysIleLeu

 2051 TACGGCCAGA TGCCACCAAG AATGCCAGGA ATGATTTCCT GAAAGAGGTG
 658 ArgProAs pAlaThrLys AsnAlaArgA snAspPheLe uLysGluVal

 2101 AAGATCATGT CGAGGCTCAA GGACCCAAAC ATCATTGGC TGCTGGCGT
 674 LysIleMetS erArgLeuLy sAspProAsn IleIleArgL euLeuGlyVal

 2151 GTGTGTGCAG GACGACCCCC TCTGCATGAT TACTGACTAC ATGGAGAACG
 691 CysValGln AspAspProI euCysMetI1 eThrAspTyr MetGluAsnGly

 2201 GCGACCTCAA CCAGTTCCCTC AGTGCCACC AGCTGGAGGA CAAGGCAGCC
 708 AspLeuAs nGlnPheLeu SerAlaHisG lnLeuGluAs pLysAlaAla

 2251 GAGGGGGCCC CTGGGGACGG GCAGGCTGCG CAGGGGCCCA CCATCAGCTA
 724 GluGlyAlaP roGlyAspG1 yGlnAlaAla GlnGlyProT hrIleSerTyr

 2301 CCCAATGCTG CTGCATGTGG CAGCCCAGAT CGCCTCCGGC ATGCGCTATC
 741 ProMetLeu LeuHisValA laAlaGlnI1 eAlaSerGly MetArgTyrLeu

 2351 TGGCCACACT CAACTTTGTA CATGGGACC TGGCCACGCG GAACTGCCCTA
 758 AlaThrLe uAsnPheVal HisArgAspL euAlaThrAr gAsnCysLeu

 2401 GTTGGGGAAA ATTCACCAC CAAAATCGCA GACTTGGCA TGAGCCGGAA
 774 ValGlyGluA snPheThrI1 eLysIleAla AspPheGlyM etSerArgAsn

 2451 CCTCTATGCT GGGGACTATT ACCGTGTGCA GGGCCGGGCA GTGCTGCCCA
 791 LeuTyrAla GlyAspTyrT yrArgValG1 nGlyArgAla ValLeuProIle

 2501 TCCGCTGGAT GCCCTGGAG TGCATCCTCA TGGGGAAAGTT CACGACTGCG
 808 ArgTrpMe tAlaTrpGlu CysIleLeuM etGlyLysPh eThrThrAla

 2551 AGTGACGTGT GGGCTTTGG TGTGACCCCTG TGGGAGGTGC TGATGCTCTG
 824 SerAspValT rpAlaPheG1 yValThrLeu TrpGluValL euMetLeuCys

 2601 TAGGGCCCAG CCCTTGGGC AGCTCACCGA CGAGCAGGTC ATCGAGAACG
 841 ArgAlaGln ProPheGlyG lnLeuThrAs pGluGlnVal IleGluAsnAla

FIGURE 2-4

2651 CGGGGGAGTT CTCGCCGAC CAGGGCCGGC AGGTGTACCT GTCCCGGCCG
858 GlyGluPh ePheArgAsp GlnGlyArgG lnValTyrLe uSerArgPro

2701 CCTGCCTGCC CGCAGGGCCT ATATGAGCTG ATGCTTCGGT GCTGGAGCCG
874 ProAlaCysP roGlnGlyLe uTyrGluLeu MetLeuArgC ysTrpSerArg

2751 GGAGTCTGAG CAGCGACCAC CCTTTCCA GCTGCATCGG TTCCCTGGCAG
891 GluSerGlu GlnArgProP roPheSerGl nLeuHisArg PheLeuAlaGlu
>>>

2801 AGGATGCACT CAACACGGTG TGAATCACAC ATCCAGCTGC CCCTCCCTCA
908 AspAlaLe uAsnThrVal

2851 GGGAGTGATC CAGGGGAAGC CAGTGACACT AAAACAAGAG GACACAATGG

2901 CACCTCTGCC CTTCCCTCC CGACAGCCCA TCACCTCTAA TAGAGGCAGT

2951 GAGACTGCAG AAGCCCCTGT CGCCCACCCA GCTGGTCCTG TGGATGGGAT

3001 CCTCTCCACC CTCCCTCTAGC CATCCCTTGG GGAAGGGTGG GGAGAAATAT

3051 AGGATAGACA CTGGACATGG CCCATTGGAG CACCTGGGCC CCACTGGACA

3101 ACACTGATTC CTGGAGAGGT GGCTGCGCCC CCAGCTTCTC TCTCCCTGTC

3151 ACACACTGGA CCCCCACTGGC TGAGAATCTG GGGGTGAGGA GGACAAGAAC

3201 GAGAGGAAAA TGTTCCTTG TGCCTGCTCC TGTACTTGTG CTCAGCTTGG

3251 GCTTCTTCCT CCTCCATCAC CTGAAACACT GGACCTGGGG GTAGCCCCGC

3301 CCCAGCCCTC AGTCACCCCCC ACTTCCCACC TGCAGTCTTG TAGCTAGAAC

3351 TTCTCTAACG CTATACGTT CTGTGGAGTA AATATTGGGA TTGGGGGGAA

3401 AGAGGGAGCA ACGGCCATA GCCTTGGGGT TGGACATCTC TAGTGTAGCT

3451 GCCACATTGA TTTTCTATA ATCACTTGGG GTTTGTACAT TTTTGGGGGG

3501 AGAGACACAG ATTTTACAC TAATATATGG ACCTAGCTTG AGGCAATT

3551 AATCCCTGC ACTAGGCAGG TAATAATAAA GGTTGAGTT TCCACAAAAA

3601 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA

FIGURE 3

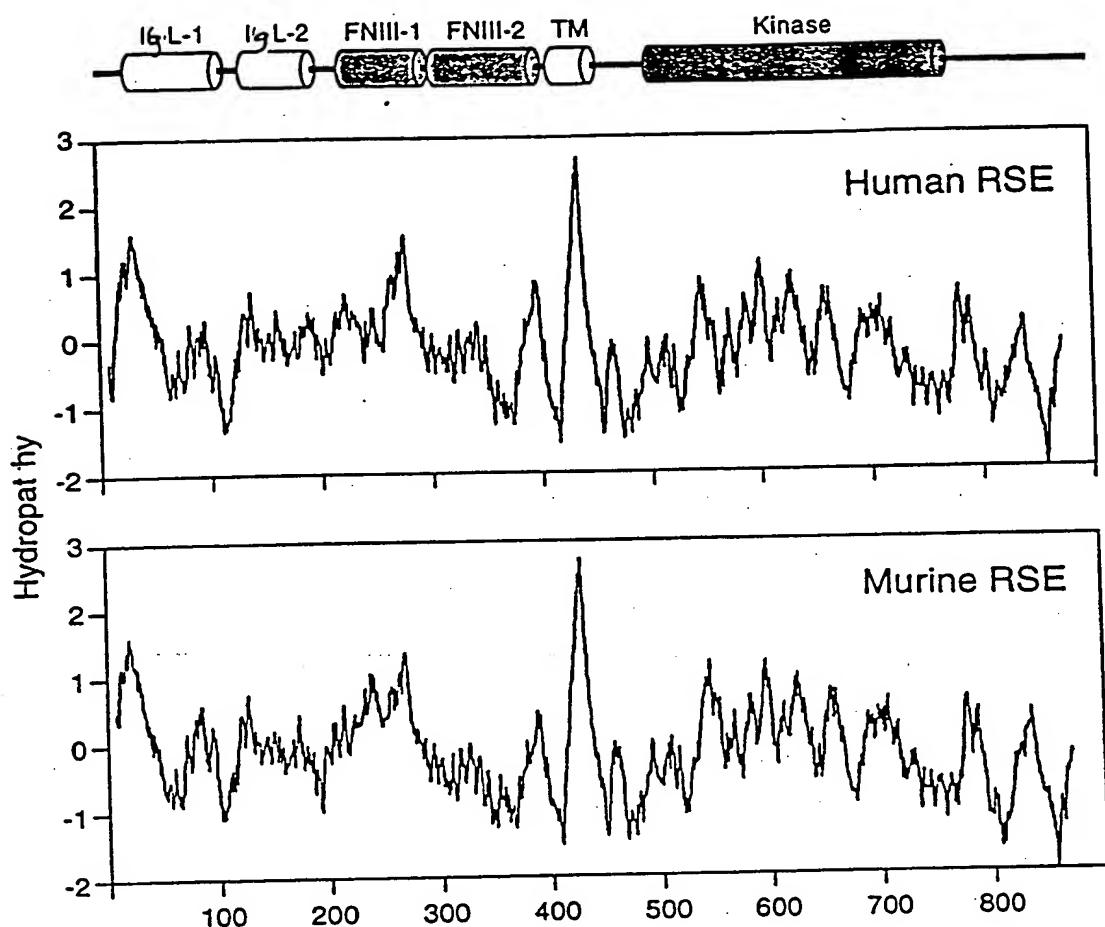


FIGURE 4 - 1
Signal Sequence

hRSE	1	M A L R - R S M G R P G L P P P L P P P P R L G U L L A A L A S L L L P E S A A A - G L K L M G A
mRSE	1	M A L R - R S M G W P G L R P - - - - - L L L A G L A S L L L P G S A A A - G L K L M G A
hAXL	1	M A H R C P R M G R V P L A - - - - - H C L A L C G W A C H A P R G T O A E - E S P F V G N
maxL	1	- - - - - M G R V P L A - - - - - H H A L C C C W G C A A H K D T O T E A G S P F V G N
* Ig-like Domain-1 *		
hRSE	49	P V K L T V S Q G Q P V K L N C S V E G M - E E P D I Q W V K D G A V V Q - - N L D O L Y I P V S E
mRSE	39	P V K M T V S Q G Q P V K L N C S V E G M - E D P D I H H M K D G T V V Q - - N A S Q V S I S I S E
hAXL	41	P G N I T G A R G L T G T L R C O L O V O G E P P E V H W L R D G O I L E L A D S T O T O V P L G E
maxL	35	P G N I T G A R G L T G T L R C E L O V O G E P P E V V W L R D G O I L E L A D N T O T O V P L G E
* Ig-like Domain-2 *		
hRSE	96	- - - Q H W I G F - - L S L K S V E R S D A G R Y W C O V E D G G E T E I S O P V H L T V E G V P F
mRSE	86	- - - H S W I G L - - L S L K S V E R S D A G L Y W C O V K D G E E T K I S O S V H L T V E G V P F
hAXL	91	D E O D D H I V V S O L R I T S L O L S D T G O Y O C L Y F L G H O T F Y S Q P G Y V G L E G L P Y
maxL	85	D W O D E H K V V S O L R I S A L O L S D A G E Y O C M Y H L E G R T F Y S O P G F V G L E G L P Y
* FN Type III Domain		
hRSE	189	V L N V T G V T O S T M F S C E A H N L K G L A S S R T A T Y H L O A L P A A P F N I T V T K L S S
mRSE	179	V L N V T G V T O R T E F S C E A R N I K G L A T S R P A I V R L O A P P A A P F N T T V T T I S S
hAXL	191	S L H V P G L N K T S S F S C E A H N A K G V T T S R T A T I T V - - L P O O P R N L H L V S R Q P
maxL	185	S L Q T P G L N K T S S F S C E A H N A K G V T T S R T A T I T V - - L P O R P R H H L H V V S R Q P
hRSE	239	S N A S V A H M P G A D G R A L L Q S C T V O V T Q A P G G H - - - - - - - - - E V L A V V V P
mRSE	229	Y N A S V A H Y P G A D G L A L L H S C T V O V A H A P G E H - - - - - - - - - E A L A V V V P
hAXL	239	T E L E V A H T P G L S G I Y P L T H C T L O A V L S D D G M G I O A G E P D P P E E P L T S O A S
maxL	233	T E L E V A H T P G L S G I Y P L T H C N L O A V L S D D G V G I H L G K S D P P E D P L T L Q V S
hRSE	278	V P P F T C L L R D C V P A T N Y S L R V R C A N A L G P S P Y A D H V P F O T K G L A P A S A P O
mRSE	268	V P P F T C L L R N L A P A T N Y S L R V R C A N A L G P S P Y G D H V P F O T K G L A P A R A P O
hAXL	289	V P P H O L R L G S L H P H T P Y H I R V A C T S S O G P S S W T H W L P V E T P E G V P L G P P E
maxL	283	V P P H O L R L E K L L P H T P Y H I R I S C S S S O G P S P W T H W L P V E T T E G V P L G P P E
hRSE	328	N L H A I R T D S G L I L E W E E E V I P E A P L E G P L G P Y K L S W V Q D N G T O D E L T V E G T
mRSE	318	N F H A I R T D S G L I L E W E E E V I P E D P G E G P L G P Y K L S W V O E N G T O D E L M V E G T
hAXL	339	N I S A T R N G S O A F Y H W O E - - P R A P L O G T L L G Y R L A Y - Q G O D T P E V L M D I G L
maxL	333	N V S A M R N G S O V L V R W O E - - P R V P L O G T L L G Y R L A Y - R G O D T P E V L M D I G L
hRSE	378	R A N L T - G W D P Q K D L I - V R V C V S - - N A V G C G P W S O P L V V - - - S S H D R A G O
mRSE	368	R A N L T - D W D P Q K D L I - L R V C A S - - N A I G D G P W S O P L V V - - - S S H D H A G R
hAXL	386	R Q E V T L E L Q G D G S V S N L T V C Y A A Y T A A G G D G P H S L P V P L E A H R P G Q A O P V H
maxL	380	T R E V T L E L R G D R P V A N L T V S Y T A Y T S A G D G P H S L P V P L E P H R P G Q O P L H
Transmembrane Domain		
hRSE	420	Q - - - G P P H S R T S H V - - P V V L G V L T A L Y T A A A L A L I L L R K R R K E T R F G Q A F
mRSE	410	Q - - - G P P H S R T S H V - - P V V L G V L T A L I T A A A L A L I L L R K R R K E T R F G Q A F
hAXL	436	Q L V K E P S T P A F S H P H W Y V L L G A V V A A C V L I L A L F L V H R R K K E T R Y G E V F
maxL	430	H L V S E P P P R A F S H P H W Y V L L G A V V A A C V L I L A L F L V H R R K K E T R Y G E V F

FIGURE 4-2

hRSE	465	D S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L G I S D E L K E K L E D V Y L I P	
mRSE	455	D S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L G I S D E L K E K L E D V Y L I P	
hAXL	486	E P T Y V E R G E L V V R Y R V R K S Y S R - - - R T T E A T L N S L G I S E E L K E K L R D V M V D	
mAXL	480	E P T Y V E R G E L V V R Y R V R K S Y S R - - - R T T E A T L N S L G I S E E L K E K L R D V M V D	
I Tyrosine Kinase Domain II			
hRSE	515	E O O F T L G R M L G K G E F G S V R E A O L K O E D G S F V K V A V K M L K A D I I I A S S D I E E	
mRSE	505	E O O F T L G R M L G K G E F G S V R E A O L K O E D G S F V K V A V K M L K A D I I I A S S D I E V	
hAXL	533	R H K V A L G K T L G E G E F G A V H E G Q L N O D D - S I L K V A V K T M K I A I C T R S E L E D	
mAXL	527	R H K V A L G K T L G E G E F G A V H E G Q L N O D D - S I L K V A V K T M K I A I C T R S E L E D	
III IV V			
hRSE	565	F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F	
mRSE	555	F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F	
hAXL	582	F L S E A V C M K E F D H P H V M R L I G V C F Q G S E R E S F P A P P V V I L P F M K H G D L H S F	
mAXL	576	F L S E A V C M K E F D H P H V M R L I G V C F Q G S D R E G F P E P V V I L P F M K H G D L H S F	
VIa VIb			
hRSE	615	L L A S R I G E N P F N L P L Q T L I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A	
mRSE	605	L L A S R I G E N P F N L P L Q T L I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A	
hAXL	632	L L Y S R L G D O P V Y L P T O M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L H	
mAXL	626	L L Y S R L G D O P V Y F L P T O M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L H	
VII VIII			
hRSE	665	E D M T V C Y A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K H L A L E S L A D N L Y T V Q S D	
mRSE	655	E D M T V C Y A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K H L A L E S L A D N L Y T V H S D	
hAXL	682	E N M S V C Y A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K H I A I E S L A D R V Y T S K S D	
mAXL	676	E N M S V C Y A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K H I A I E S L A D R V Y T S K S D	
IX X			
hRSE	715	V W A F G V T M H E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E D V Y D L	
mRSE	705	V W A F G V T M H E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E E V Y D L	
hAXL	732	V W S F G V T M H E I A T R G Q T P Y P G Y E N S E I Y D Y L R O G N R L K O P A D C L D G L Y A L	
mAXL	726	V W S F G V T M H E I A T R G Q T P Y P G Y E N S E I Y D Y L R O G N R L K O P V D F L D G L Y S L	
XII			
hRSE	765	M Y Q C H S A D P K O R P S F T C L R M E L E N I L G O L S V L S A S O D P L Y I N H I E R A E E P T	
mRSE	755	M Y Q C H S A D P K O R P S F T C L R M E L E N I L G H L S V L S T S O D P L Y I N H I E R A E O P T	
hAXL	782	M S R C H E L N P Q D R P S F T E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G G Y P	
mAXL	776	M S R C H E L N P R D R P S F A E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G S H L	
1815 A G G S L E L P G R D O P Y S G A G D G S G M G A V G G T P S D C R Y I L T P G G L A E O P G O A E			
805 E S G S P E L H C G E R S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S E S P G O L E			
832 E P P G A A G G A D P P T Q P D P K D S C S C L T A A E V H P A G R Y V L C P S T - T P S P A O P A			
826 E P R G A A G G A D P P T Q P D P K D S C S C L T A A D V H S A G R Y V L C P S T - A P G P T L S A			
865 H Q P E S P L N E T O R L L L L O O G L L P H S S C			
855 Q Q P E S P L N E N O R L L L L O O G L L P H S S C			
881 - D R G S P A A P G O - - - E D G A - - - - -			
875 - D R G C P A P P G O - - - E D G A - - - - -			

FIGURE 5

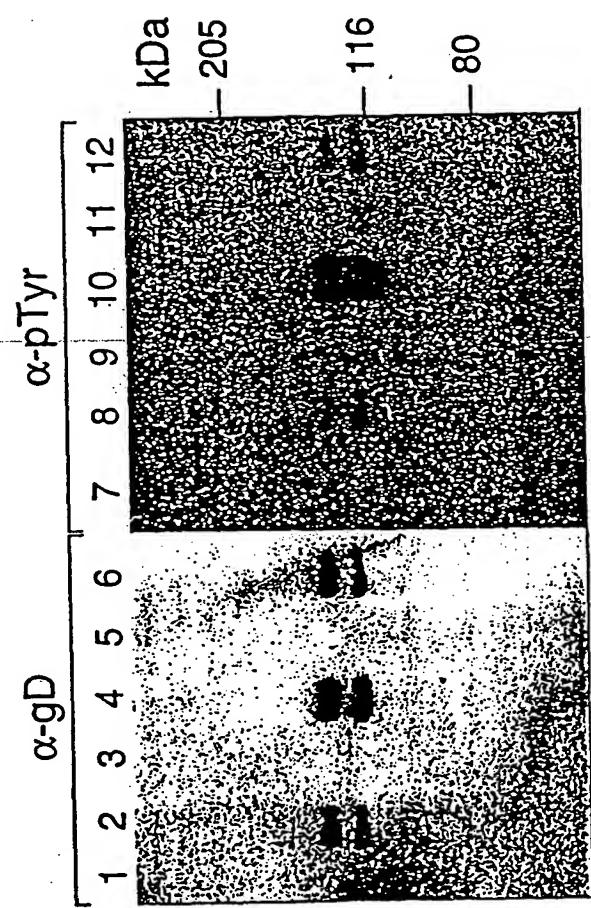
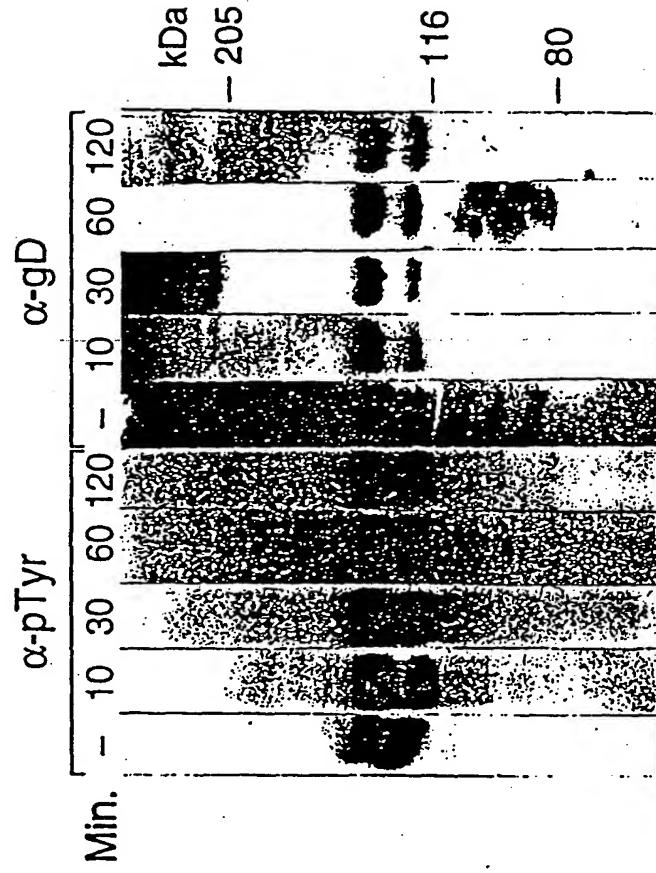


FIGURE 6



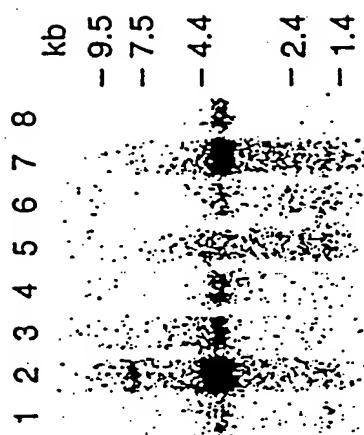


FIGURE 1A



FIGURE 1B

FIGURE 8 A

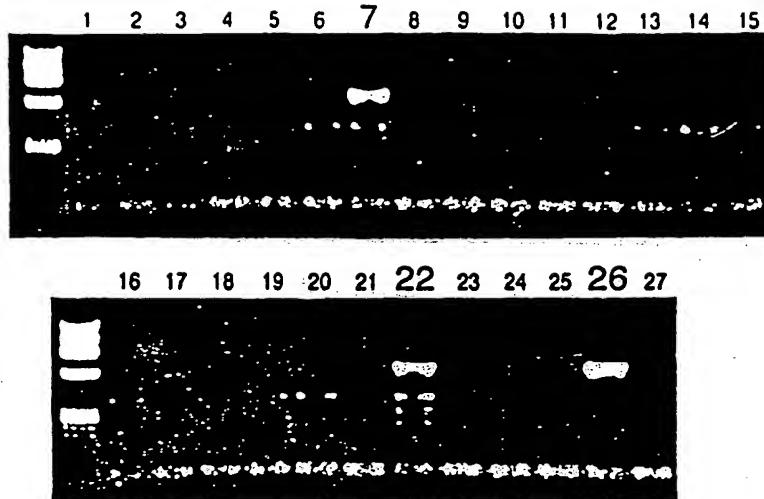


FIGURE 8B

CHROMOSOME CONTENT OF SOMATIC CELL HYBRID PANEL

FIGURE 9.

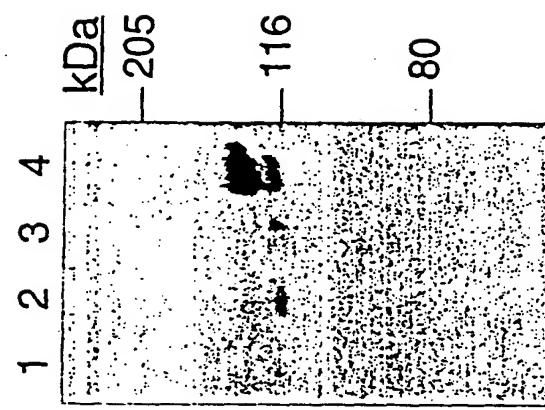


FIGURE 10A.

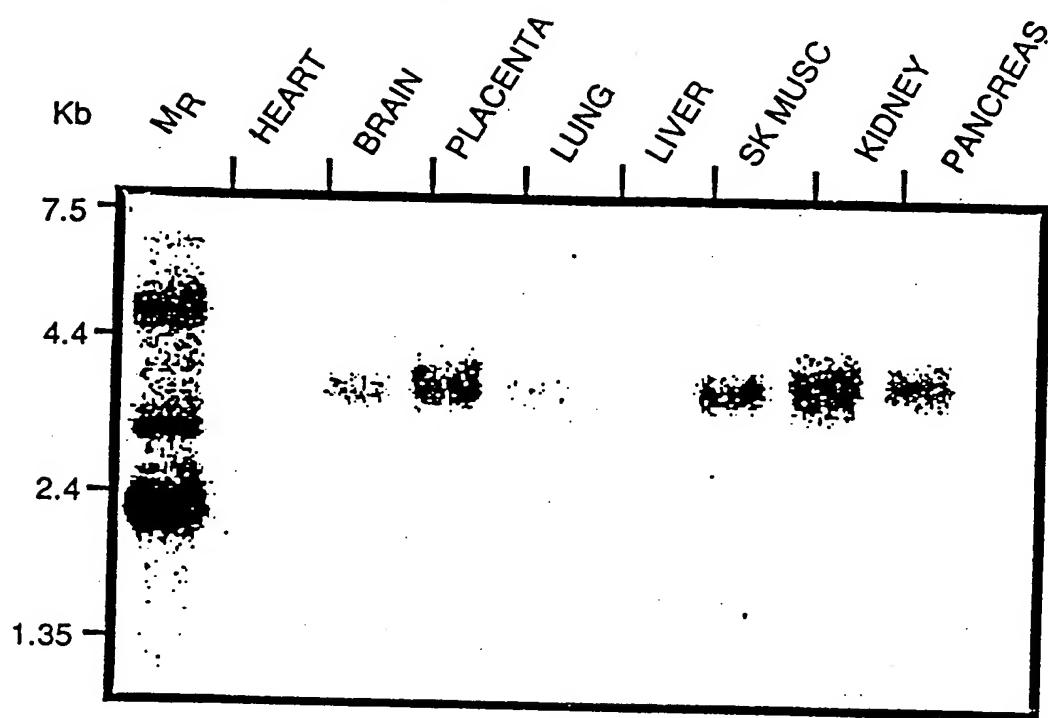


FIGURE 10 B.

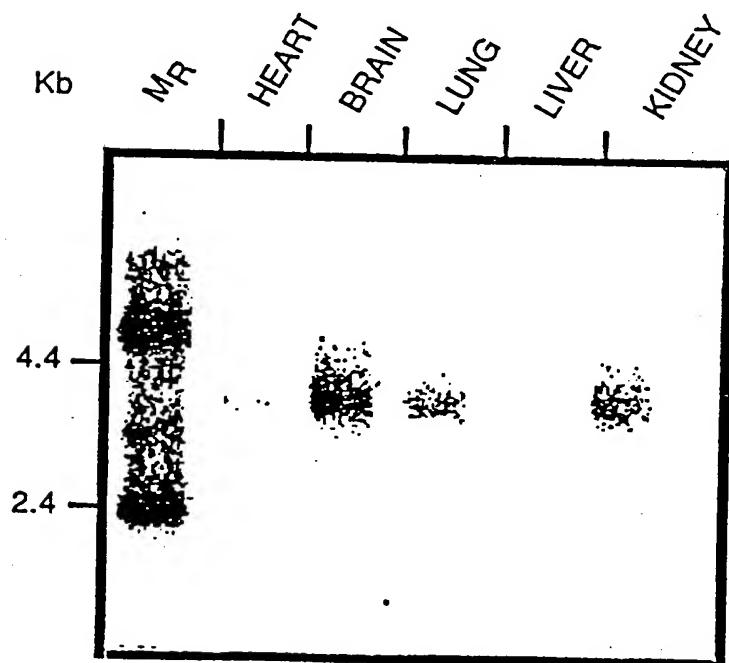


FIGURE II A

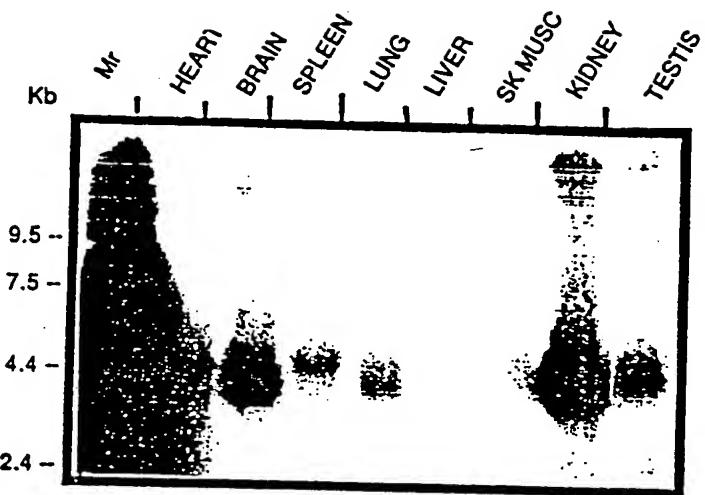


FIGURE II B

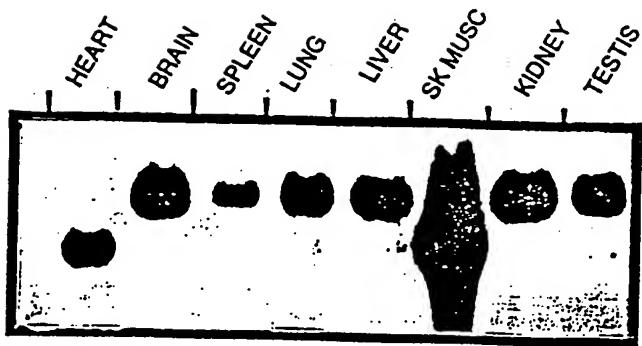


FIGURE 12A
HUMAN -ve STRAND

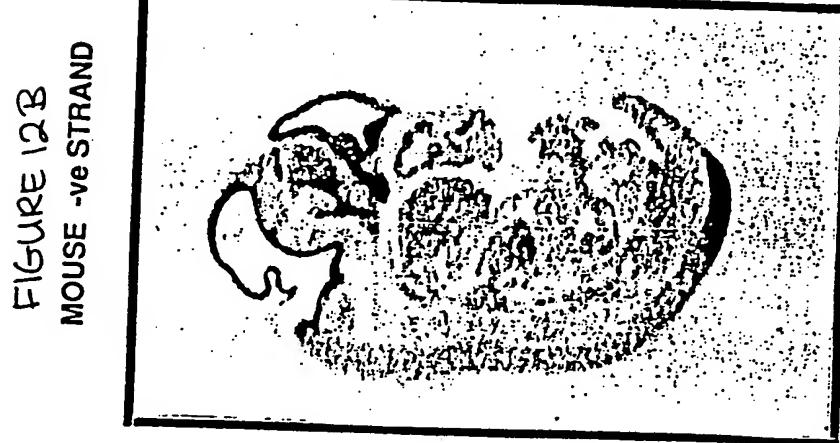
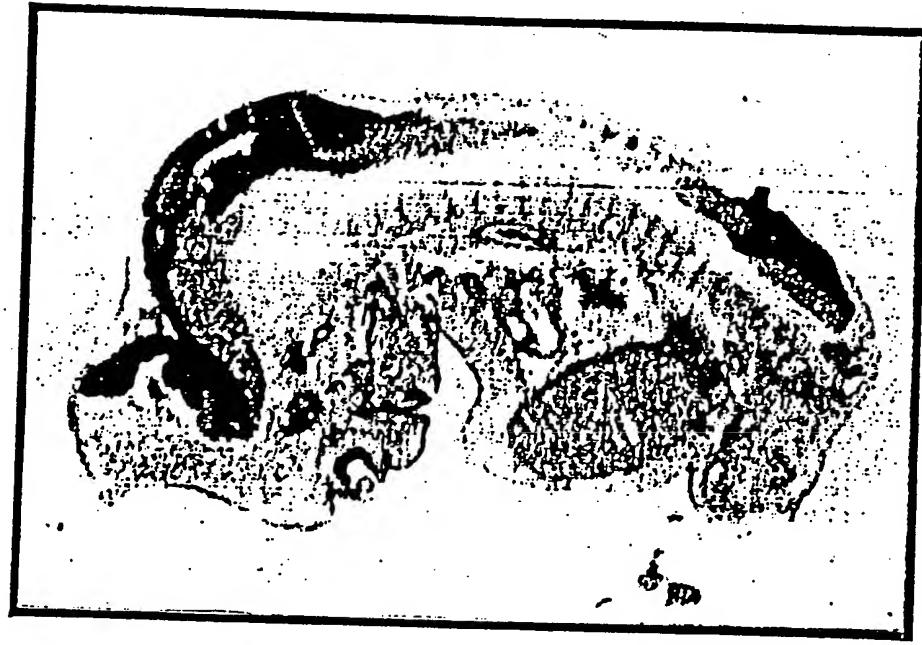


FIGURE 12B
MOUSE -ve STRAND

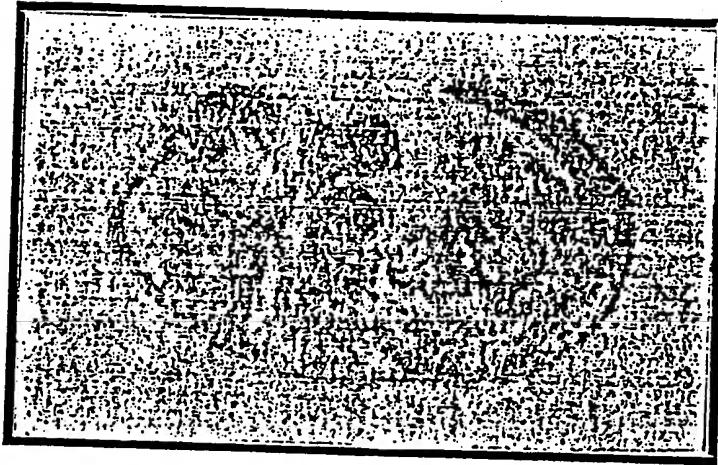


FIGURE 12C
MOUSE +ve STRAND